REMARKS

Applicants are submitting this amendment in order to respond to the Examiner's requirement. In response to the requirement to choose a particular species as part of the restriction requirement, Applicants select the species that is SEQ ID NO: 1. Applicants elect the claims of Group IV and SEQ ID NO: 1 with traverse.

Applicants wish to reiterate their claim to the benefit of their German priority date of 10 July 2002 pursuant to the International Convention. A certified copy of German Patent Application 102 31 297.4 filed 10 July 2002 has been made of record in PCT/DE 2003/002290 filed 8 July 2003 of which the instant application is the US national Phase. The Examiner is respectfully requested to acknowledge Applicants' perfected right of priority.

Applicants are enclosing herewith an additional certified copy of the German Priority Document together with a translator's certification that the German Priority Document and the International Patent Application PCT/DE 2003/002290 filed 8 July 2003, filed in German are word for word identical, and that the English language text that is the present US Application is an accurate translation of these German patent documents. These submissions are relevant to antedating the BELL et al reference, cited by the Examiner as a basis for the restriction requirement, thereby removing BELL et al as an effective prior art reference. Applicants are providing further explanation later on in this amendment.

Applicants have added new independent claim 28 and new dependent claim 29. Antecedent basis for the new claims may be found in the specification on page 2, line 17 to page 4, line 18.

The Examiner has given Applicants an onerous requirement for restriction (lack of unity of invention) and has divided up the claims into four groups. The claims of Group I, claims 1 to 10, are directed to the polynucleotides of SEQ ID NOS: 1 through 5, fragments of the SerA gene (gene expressing 3-phosphoglycerate dehydrogenase) especially the SerA isolated from Corynebacterium glutamicum, as well as expression cassettes and vectors containing the gene fragments. The claims of Group II, claims 11 through 19, are directed to the deregulated 3-phosphoglycerate dehydrogenase that is expressed by these gene fragments. The claims of Group III, claims 20 to 26, are directed to microorganisms transformed with a gene fragment according to the claim so if Group I, and the sole claim in Group IV, claim 27, is directed to a method for the biological production of L-serine using a transformed microorganism according to the claim of Group III, in a culture medium to over-produce L-serine, without the drawback of feedback inhibition.

The Examiner argues first of all that restriction among the four groups is proper because there is no common technical feature that links all of the claims. The Examiner does not agree that the fact that the gene fragment of Group I has been modified to remove the regulatory portion of SerA where the allosteric site that binds L-serine is located is a sufficient basis to link all four of the groups even though the 3-phosphoglycerate dehydrogenase

of Group II is expressed by this very same gene fragment, and even though the microorganisms of Group III, and the method of producing L-serine of Group IV, using the microorganisms of Group III are linked as well to the claims of Group I since the microorganisms have all been transformed with a gene fragment according to the claims of Group I. The Examiner has cited the BELL et al reference, Eur. J. Biochem., 269, 4176 to 4184 (2002) for its disclosure that the serine binding region of 3-phosphoglycerate dehydrogenase is at the C-terminal end of the enzyme, and that it is known this is the region with the allosteric binding site for L-serine, and that when L-serine binds to this site, feedback inhibition results to reduce the yield of L-serine. The Examiner further argues that the reference discloses that mutations may be induced in this region of the gene expressing the enzyme to remove the problem of feedback inhibition. The Examiner then concludes that it would be obvious to create a mutation in the region of the polynucleotide expressing the 3-phosphoglycerate dehydrogenase to deactivate the allosteric binding site with the expected result of overproduction of L-serine. Thus the Examiner finds no novel technical feature binding all four groups of claims.

Applicants do not agree with the Examiner's argument. First of all the Eur. J. Biochem., 269, 4176 to 4184 (2002) was first cited in the International Search report from the European Patent Office. According to the European Search Report the publication date of the BELL et al reference was September of 2002, after the Applicants' German priority date of 10 July 2002 for

German Patent Application 102 31 297.4. Applicants are providing a certified copy of the German priority document and a certification by Andrew Wilford, Esq., that the specification in the International Application and the specification in the German Priority Document 102 31 297.4 filed 10 July 2002 are identical. Since Applicants are entitled to their 10 July 2002 German priority date as their date of constructive reduction to practice of the presently claimed invention, Applicants have antedated the BELL et al reference and the Examiner should no longer apply BELL et al as a basis to attack the unity of invention among the claims of Groups I through IV. All of the claims are related to a deregulated 3-phosphoglycerate dehydrogenase having a number of amino acids at the C-terminal deleted so as to provide an enzyme that does not suffer from the disadvantage of feedback inhibition, which will cut down on the yield of L-serine obtained in its microbiological preparation from carbohydrates, fats and oils, fatty acids, fatty alcohols or organic acids. Either the claims are directed to the 3-phosphoglycerate dehydrogenase having reduced feedback inhibition in the synthesis of L-Serine or the claims are directed to polynucleotides expressing this enzyme or to a microorganism containing the polynucleotide expressing this enzyme, or to a method of producing L-serine by using a microorganism containing the polynucleotide expressing this enzyme. Thus there is a common technical feature linking all of the claims in this application and the Examiner should not maintain his restriction requirement.

However, even if the BELL et al reference were effective prior art in the examination of this application, Applicants still do not believe that the reference discloses the same common technical feature that Applicants disclose in the present application. Applicants refer to page 4, central paragraph, of the specification, which discloses that the novel 3-phosphoglycerate dehydrogenases of the present invention must not only have reduced feedback inhibition, but at the same time retain their strong enzymatic activity to catalyze the early process steps in the synthesis of L-serine from carbohydrates. According to the central paragraph of page 3 of the application, other prior art was known at the time the present application was filed disclosing that the C-terminal of 3-phosphoglycerate dehydrogenase of E Coli, not Corynebacterium glutamicum, contained the allosteric binding site for L-serine, and that if this region in the gene is completely deleted, or at least altered, that the problem of feedback inhibition may be overcome. However, the resulting modified 3-phosphoglycerate dehydrogenase has much less enzymatic activity. Thus Applicants alone obtain a 3-phosphoglycerate dehydrogenase with reduced feedback inhibition and with retained good enzymatic activity. This combination provides the common technical feature linking all of the claims of Groups I through IV.

Applicants have provisionally elected to prosecute the claims of Group IV, and traverse the restriction requirement. The Examiner has made it clear that if Applicants elect to prosecute the claims of Groups I through II, there is a further part to the

requirement for restriction. The Examiner believes that there is no common structural feature linking all of the polynucleotides of SEQ ID NOS 1 through 5 and no common technical feature linking all of the polypeptides of SEQ ID NOS: 7 through 11. Thus the Examiner argues that Applicants have to select one of these sequences and restrict the invention to one of these individual sequences. Applicants believe that this requirement is particularly onerous and unfair. Of course all of the polynucleotides of SEQ ID NOS: 1 through 5 are fragments of the naturally occurring polynucleotide of SEQ ID NO: 6. All of the SEQ ID NOS: 1 through 5 have varying amounts of nucleotides cut off from the C-terminal and the remainder of the polynucleotide is the same for all five polynucleotides. The same is true for the polypeptides of SEQ ID NOS: 7 through 11 which are fragments of the naturally occurring peptide of SEQ ID NO: 12. All of the polypeptides of SEQ ID NOS: 7 through 11 have the first 319 amino acids in common. SEQ ID NO: 11 terminates at that point. SEQ ID NO: 10 terminates at amino acid 325; SEQ ID NO: 7 terminates at amino acid 333; SEQ ID NO: 9 terminates at amino acid 342; and SEQ ID NO:8 terminates at amino acid 451. Therefore there is a good deal of structure in common among all of the polypeptides of SEQ ID NOS: 7 through 11 and the polynucleotides of SEQ ID NOS: 1 through 5 that express these polypeptides and so there is no justification for the Examiner to argue that each of these polypeptides or polynucleotide is a separate invention and to refuse to examine all of the polynucleotides in the present application.

Applicants do not believe that they are legally required to accept the Examiner's invitation to state on the record that all of the SEQ ID NOS: 7 through 11 have equivalent activity and so the polypeptides of SEQ ID NOS 7 through 11 are all equivalent to one another and the polynucleotides of SEQ ID NOS: 1 through 5, expressing those polypeptides, are all equivalent to one another. It may well be that the polypeptide that is SEQ ID NO: 7 has far and away the best activity. See page 6, lines 6 through 8 of the specification which indicates that the polynucleotide of SEQ ID NO: 1 which codes for a 3-phosphopolyglycerate dehydrogenase of SEQ ID NO: 7 is the most advantageous. Nonetheless the fact that the overwhelming majority of the polynucleotides of SEQ ID NOS 1 through 5 are structurally identical so that a large part of each polynucleotide has a structural nucleus in common, provides a strong legal basis for Applicants' argument that all of the polynucleotides of SEQ ID NOS 1 through 5 should be examined together.

In the present response Applicants have included a subgeneric claim 28 with all five of the new polynucleotides. Once again all of these sequences have in large part a common structure, all of the species are directed to a deregulated 3-phosphoglycerate with reduced feedback inhibition that would cut down on the yield of L-serine from the carbohydrate starting material, yet at the

same time the deregulated 3-phosphoglycerate has good enzymatic activity to facilitate the conversion of carbohydrates to L-serine, and so all of the species should be examined together in one application.

Applicants await further action.

K.F. Ross P.C.

By: Jonathan Myers, 26,963
Attorney for Applicant

er
30 July 2008
5683 Riverdale Avenue Box 900
Bronx, NY 10471-0900
Cust. No.: 535
Tel: 718 884-6600
Fax: 718 601-1099
Email: *email@kfrpc.com*

Enclosures: Translator's Certificate
Transmittal of Priority Papers
Certified German Priority Document
Three Month Extension Request
PTO-2038